

Figure 1

Figure 2A

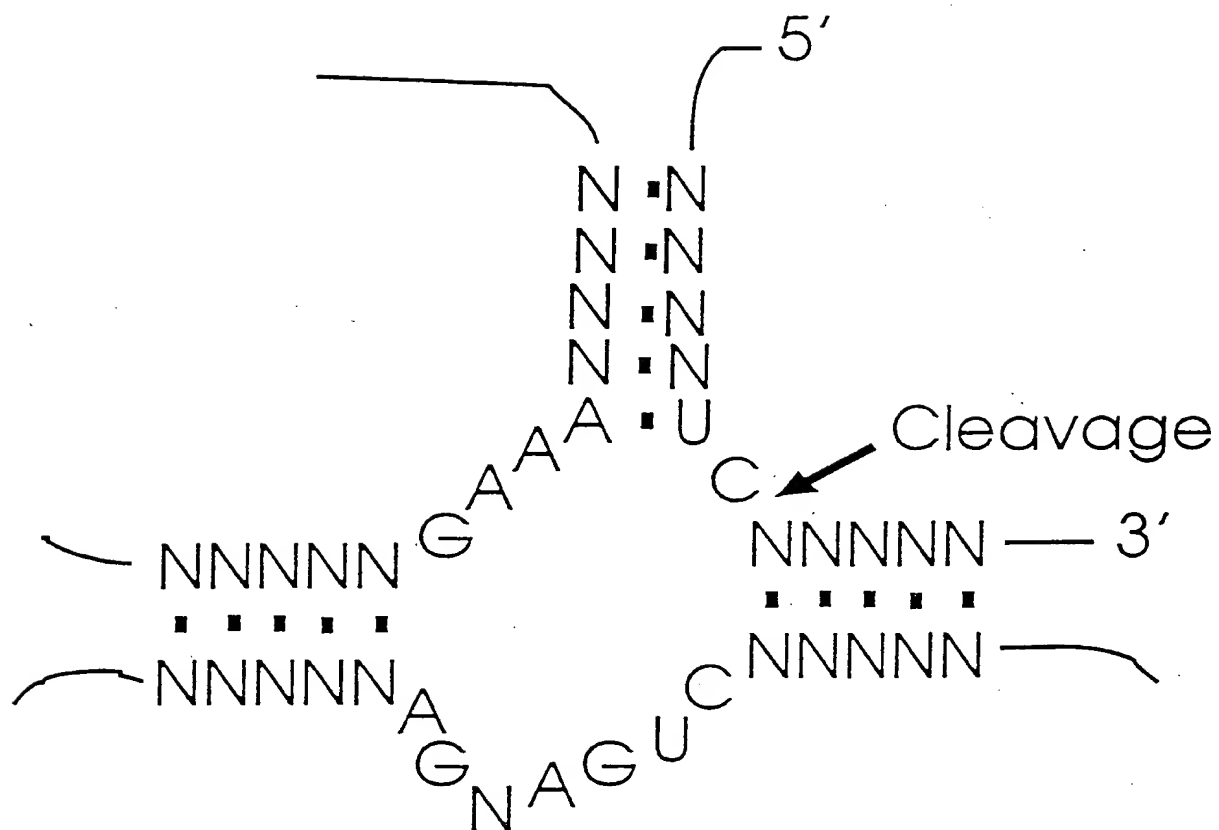


Figure 2B

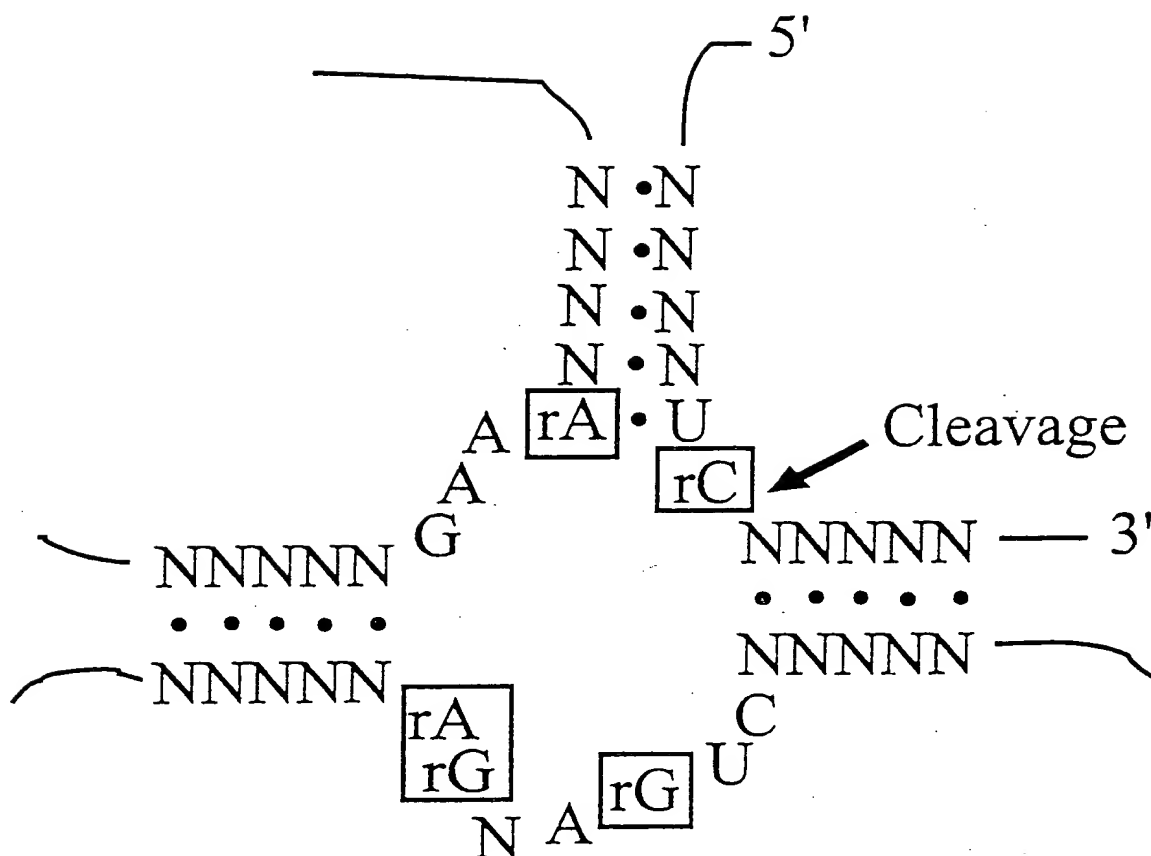
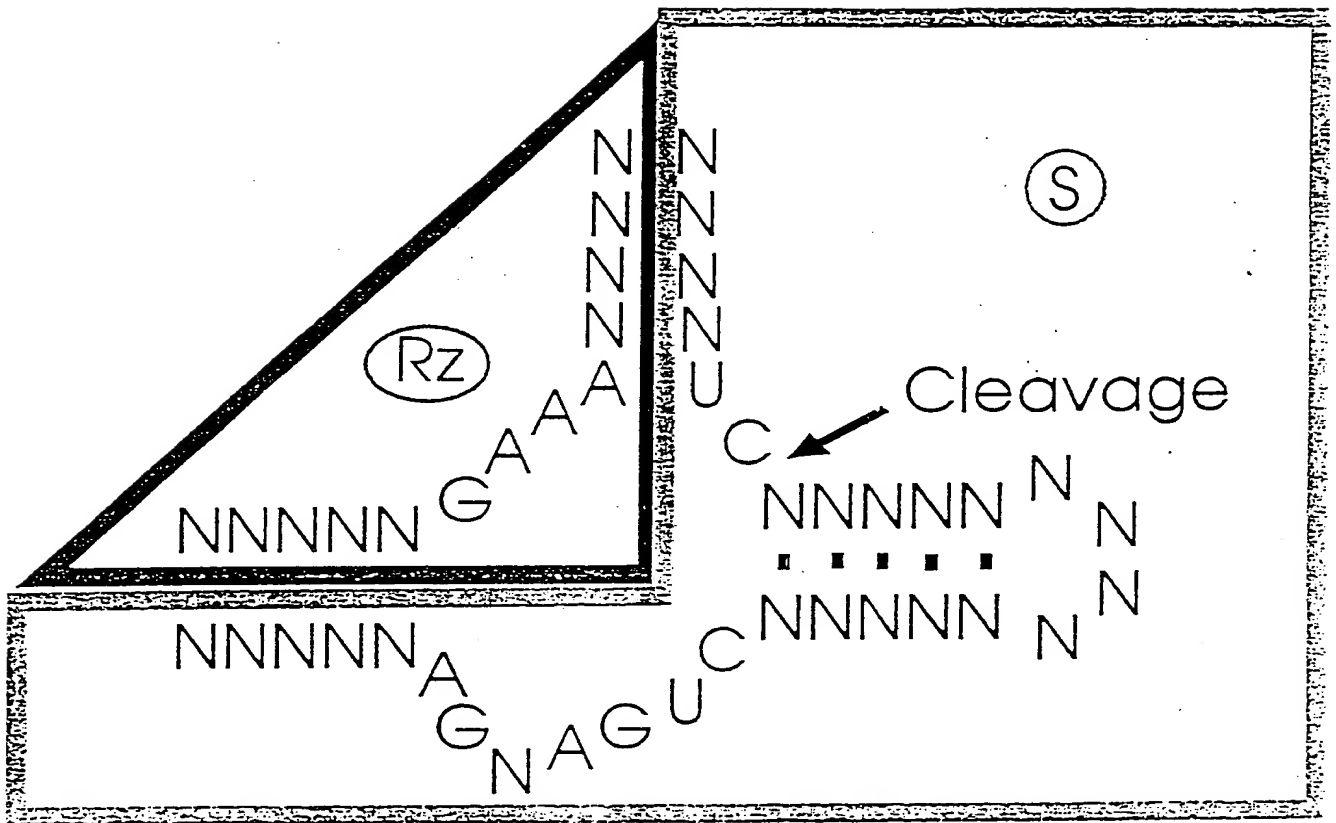


Figure 3

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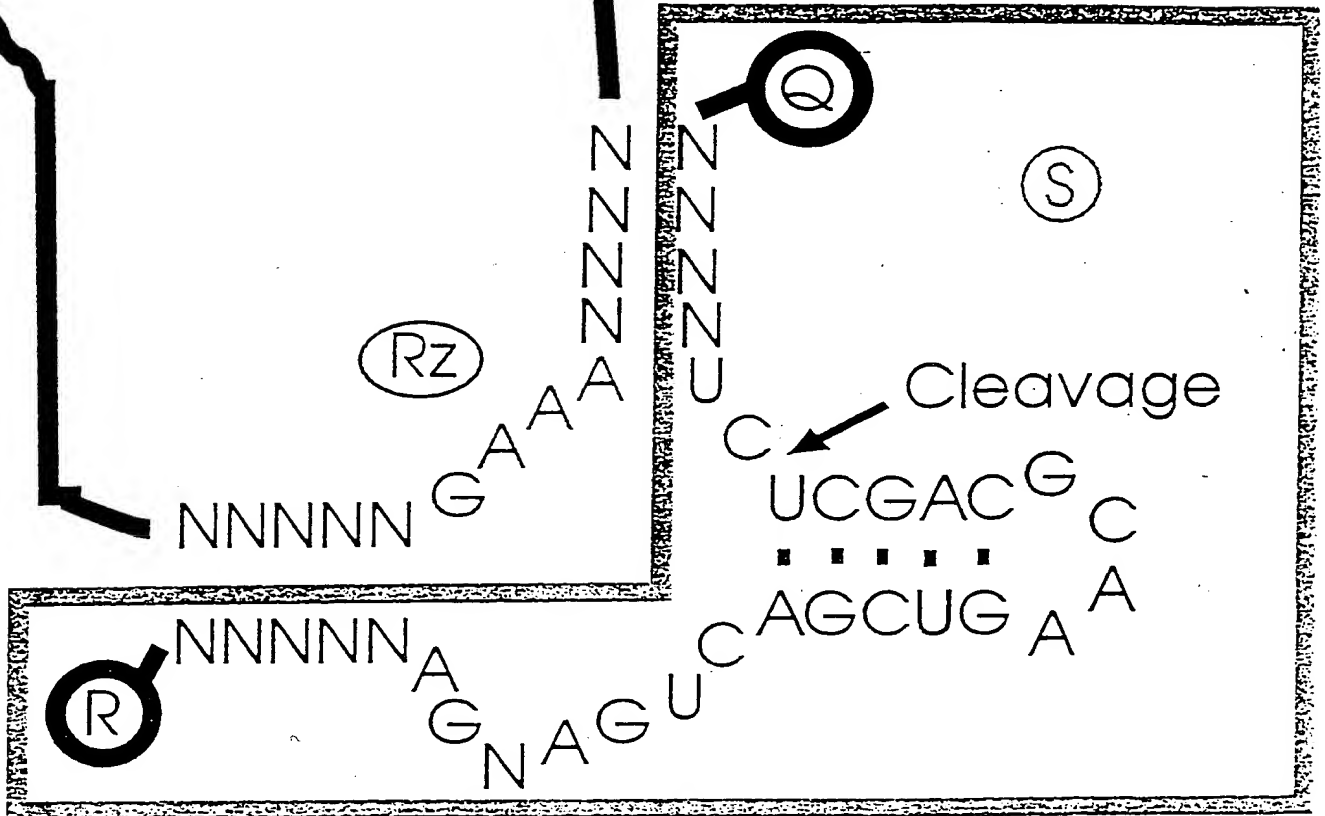
Figure 4A

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RNA

3'

5'



R = FAM
HEX
TET
ALEXA

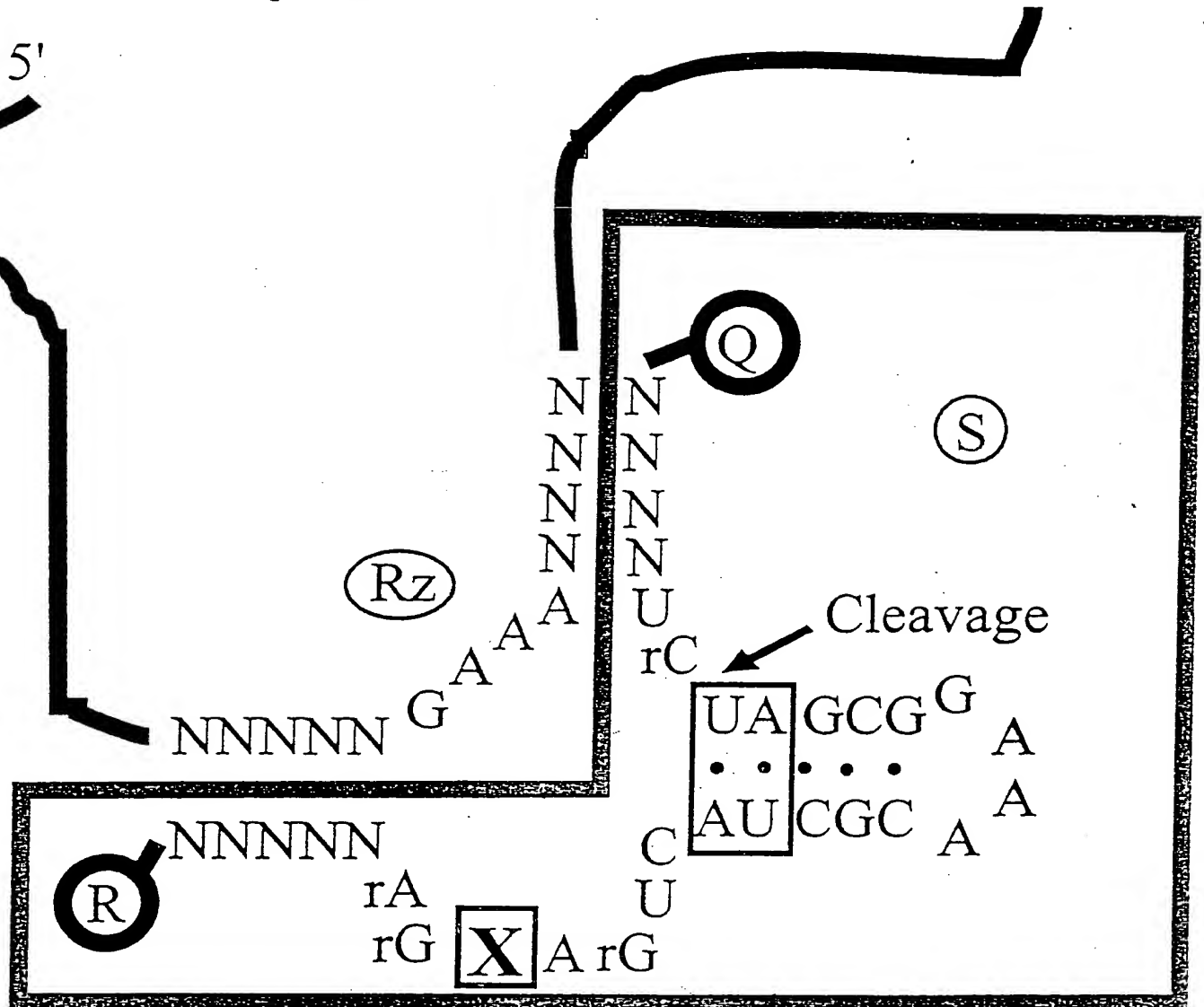
Q = TAMRA
CY-5
DABCYL
LCR
etc.

Figure 4B

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3'

5'



R = FAM
HEX
TET
ALEXA

Q = TAMRA
CY-5
DABCYL
LCR

etc.

X = Pyridin-4-one

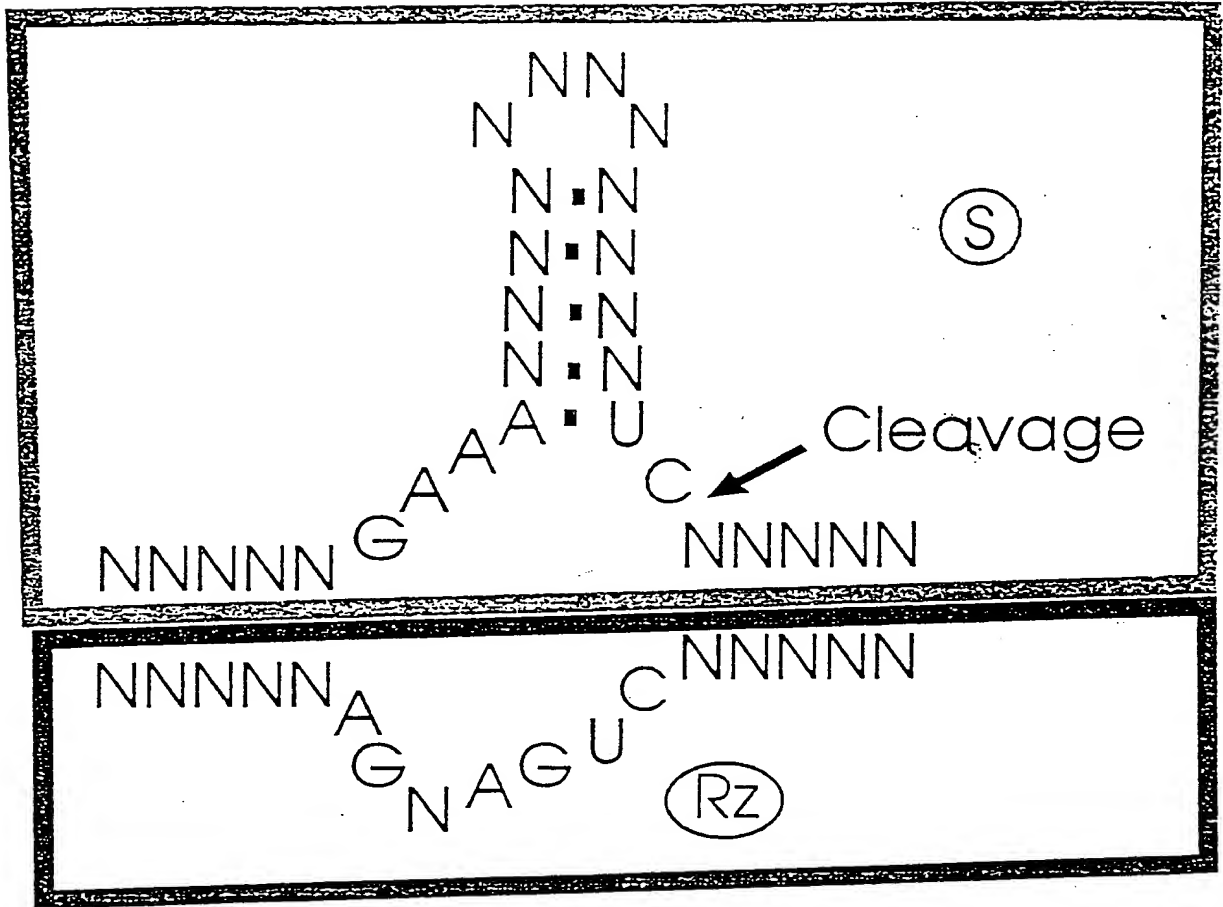
r = essential ribonucleotides

important: no (C,U)-A dinucleotide in loop

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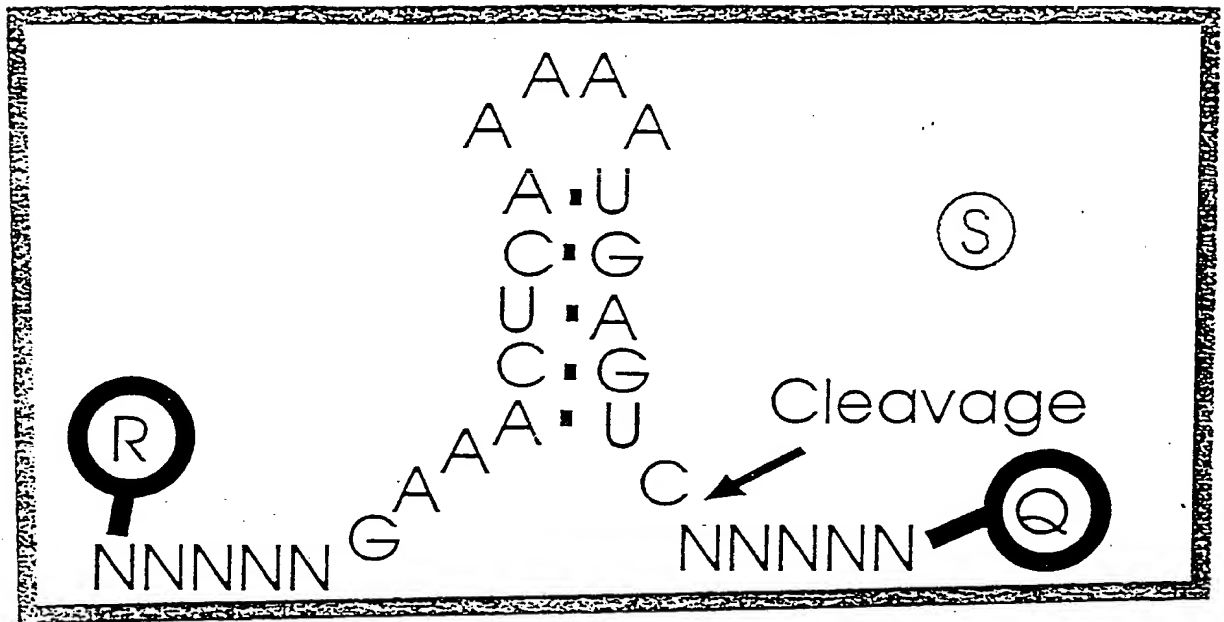
Figure 5



2050E0 6T52E660

Figure 6

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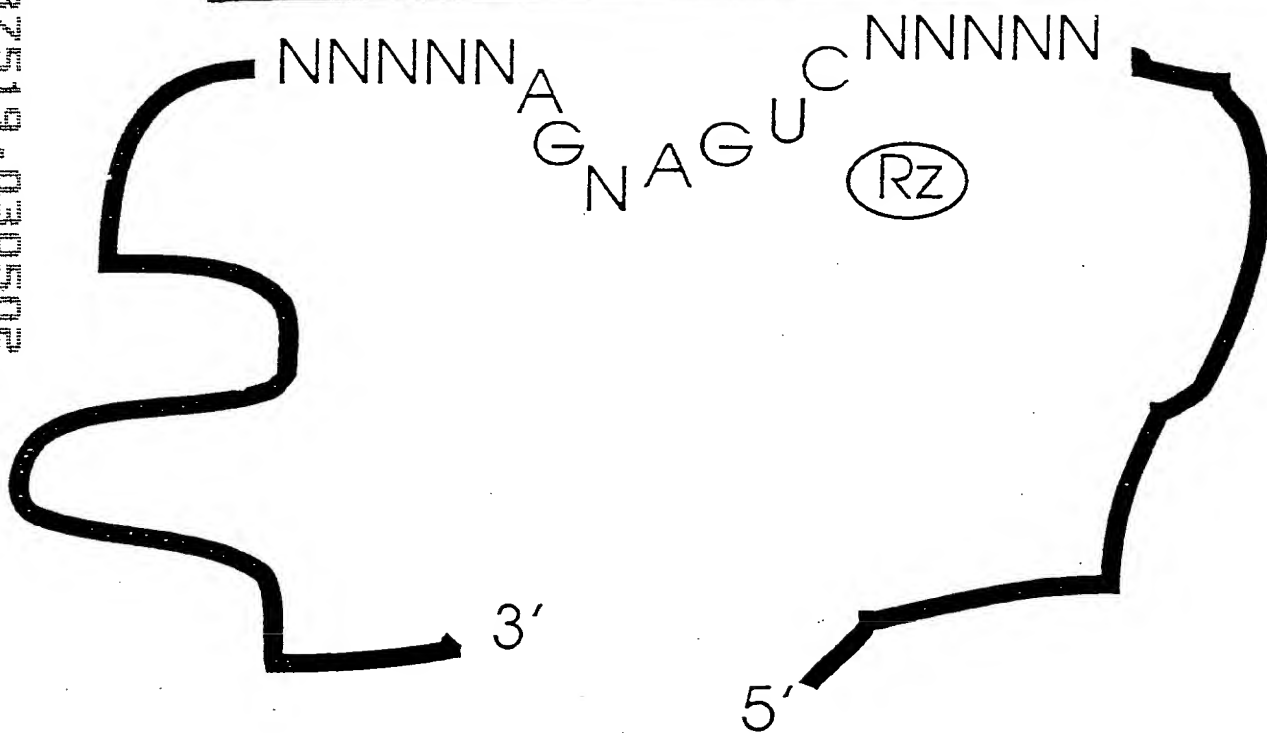
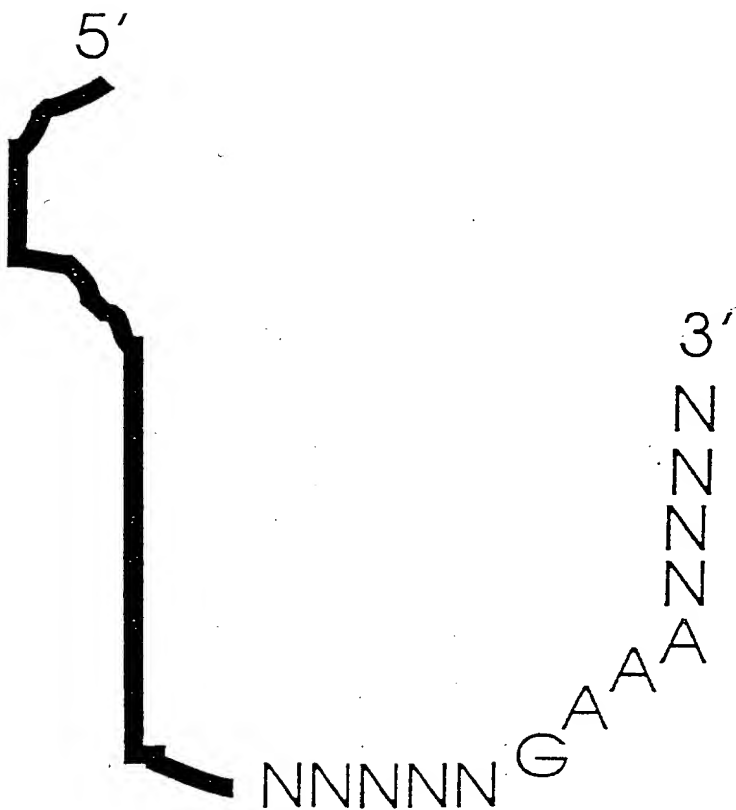
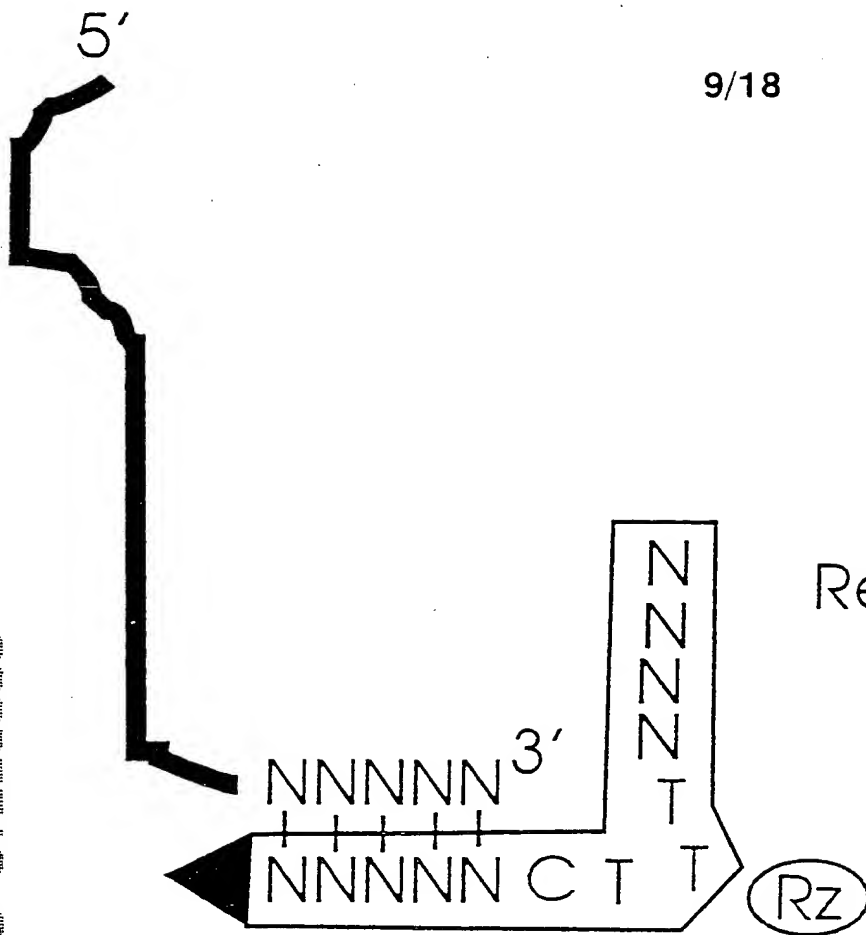


Figure 7

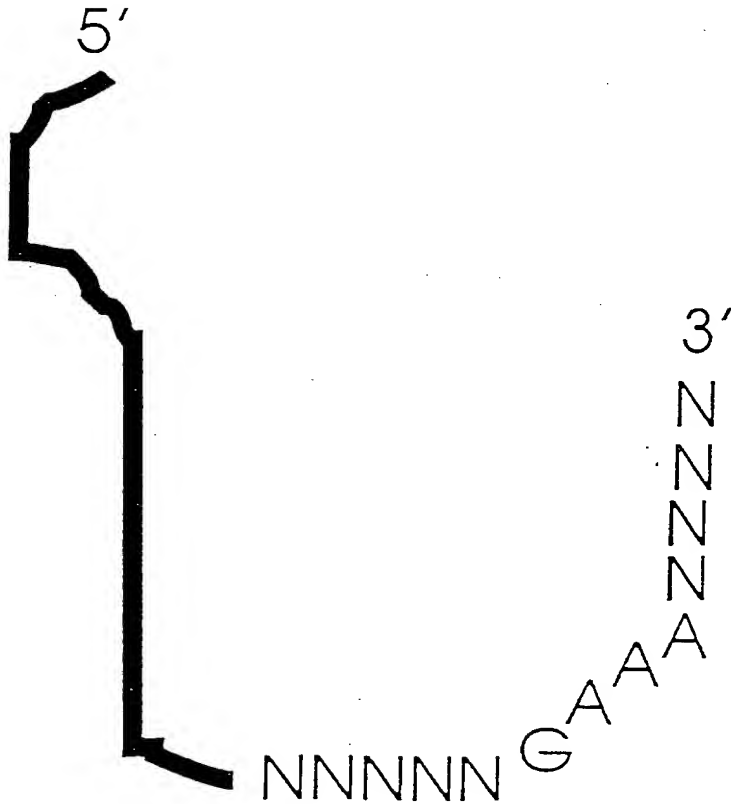
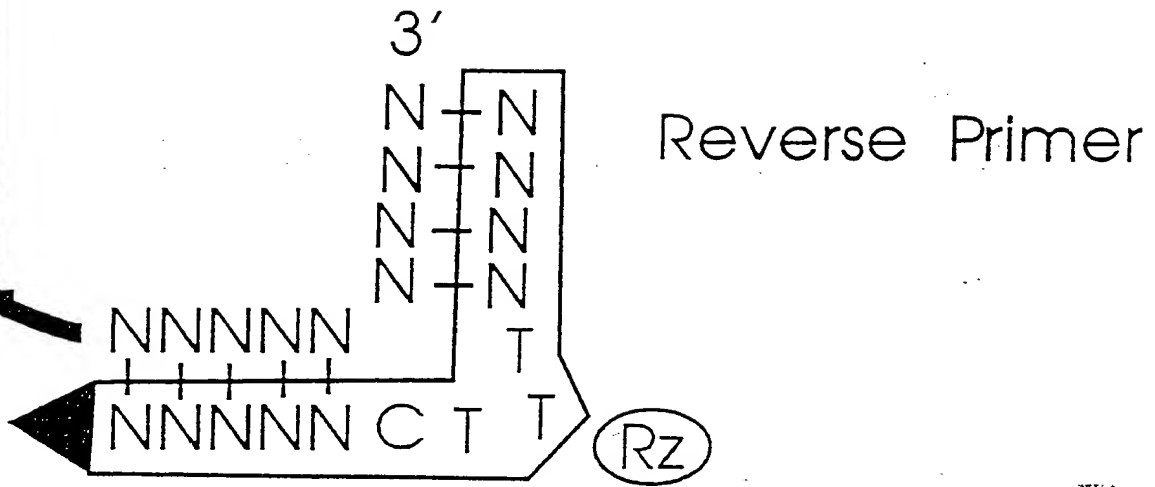
Reverse Primer

0937519.030502



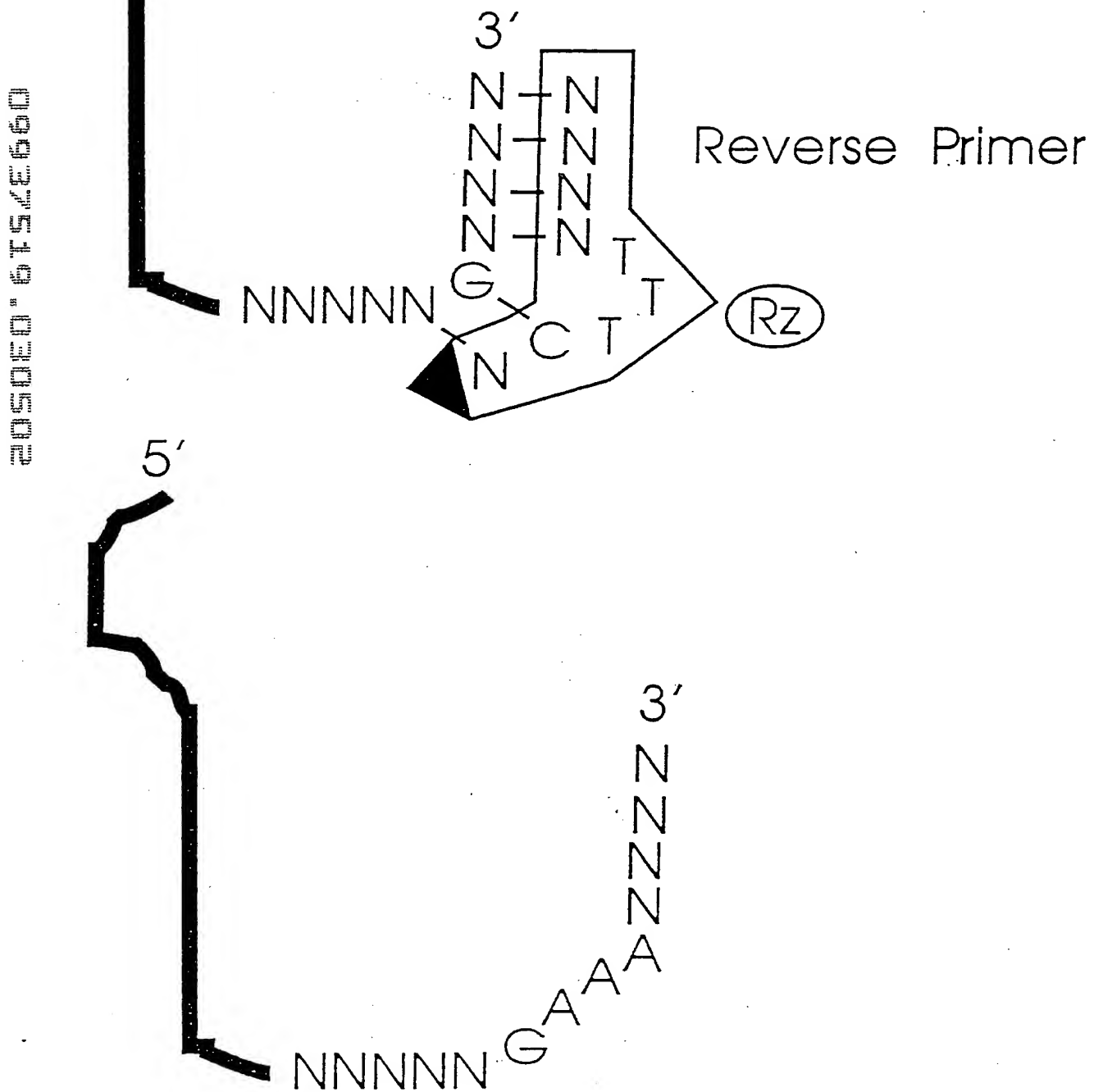
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Figure 8



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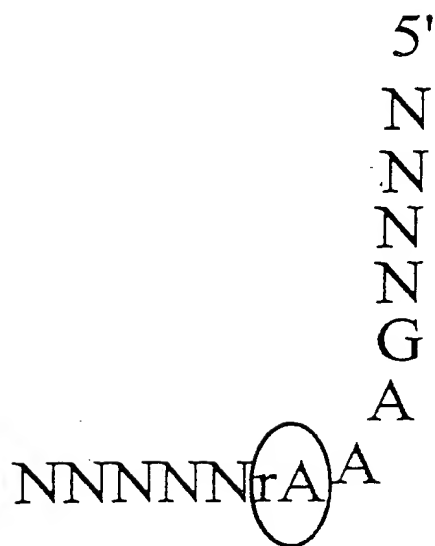
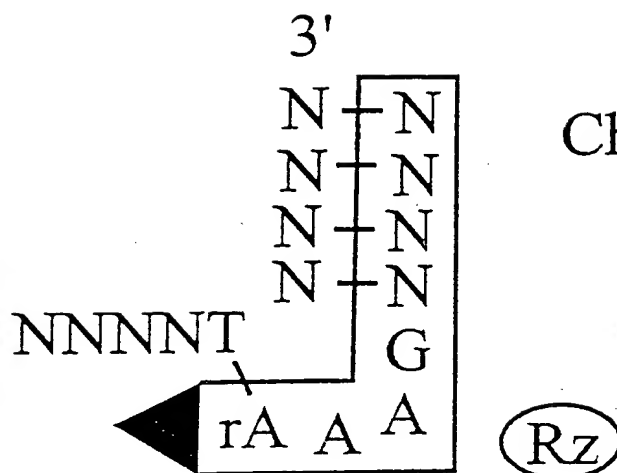
Figure 9



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Figure 10

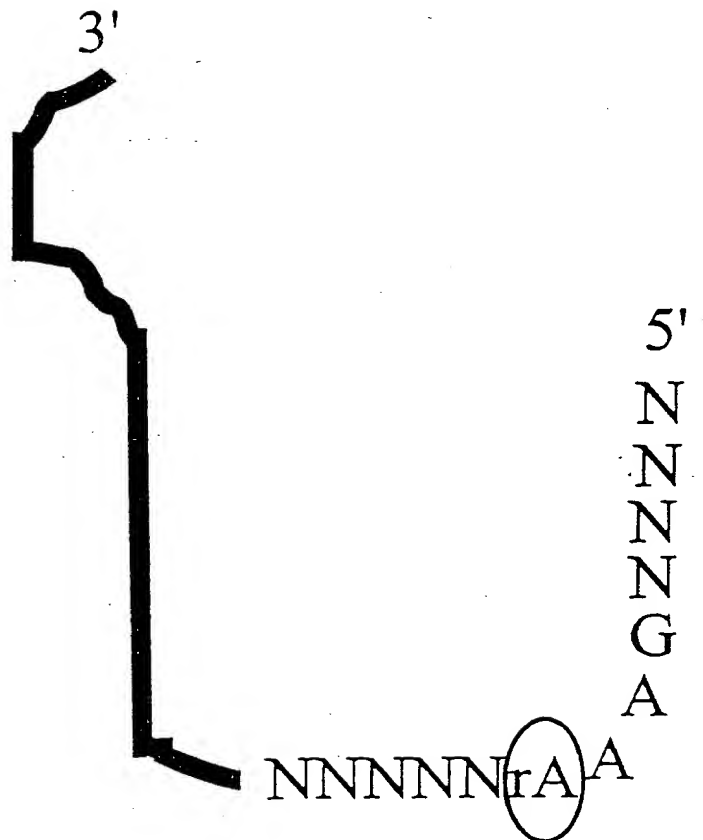
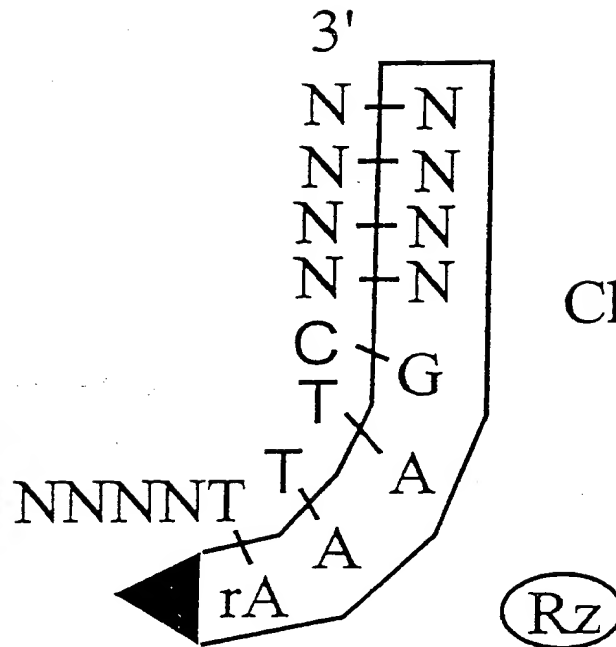
Chimeric Primer



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Figure 11

Chimeric Primer



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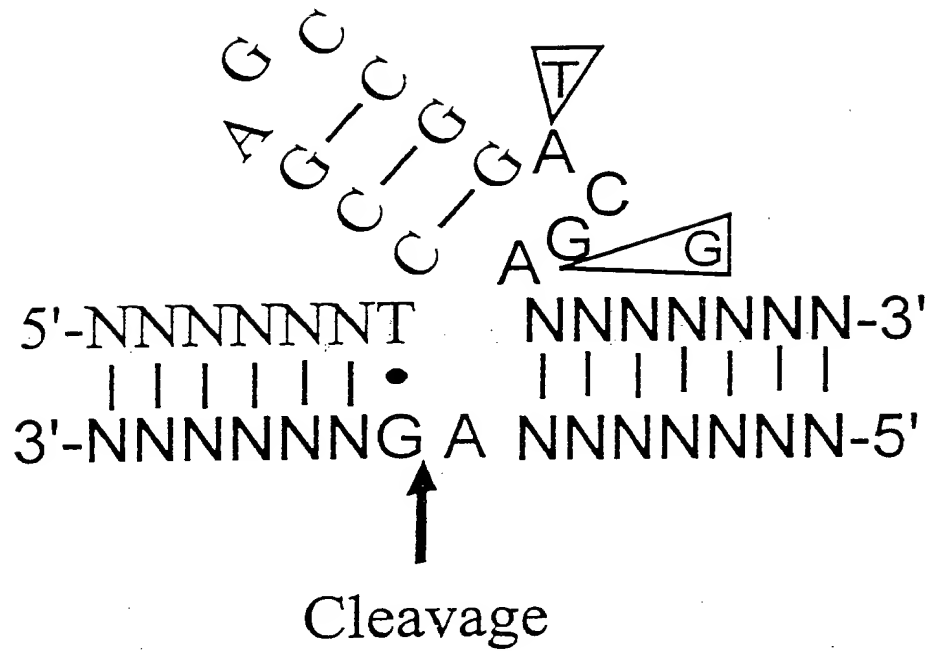


Figure 12

DNA-zyme: Prototype A

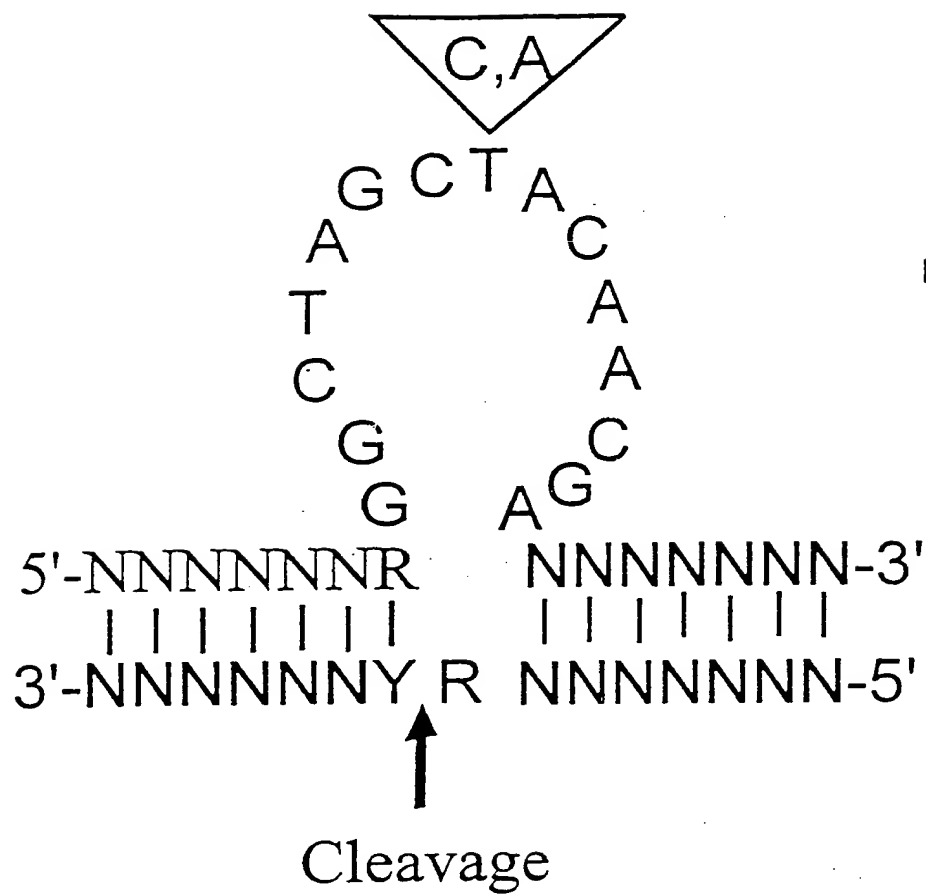
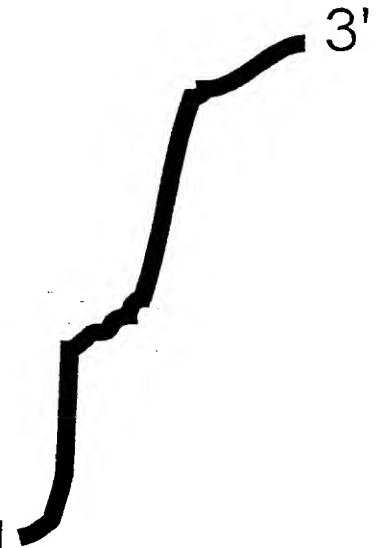
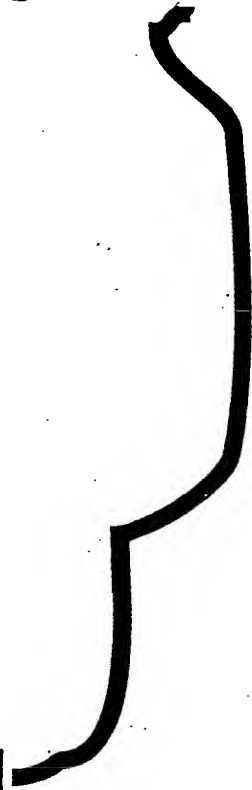


Figure 13

DNA-zyme: Prototype B

Figure 14

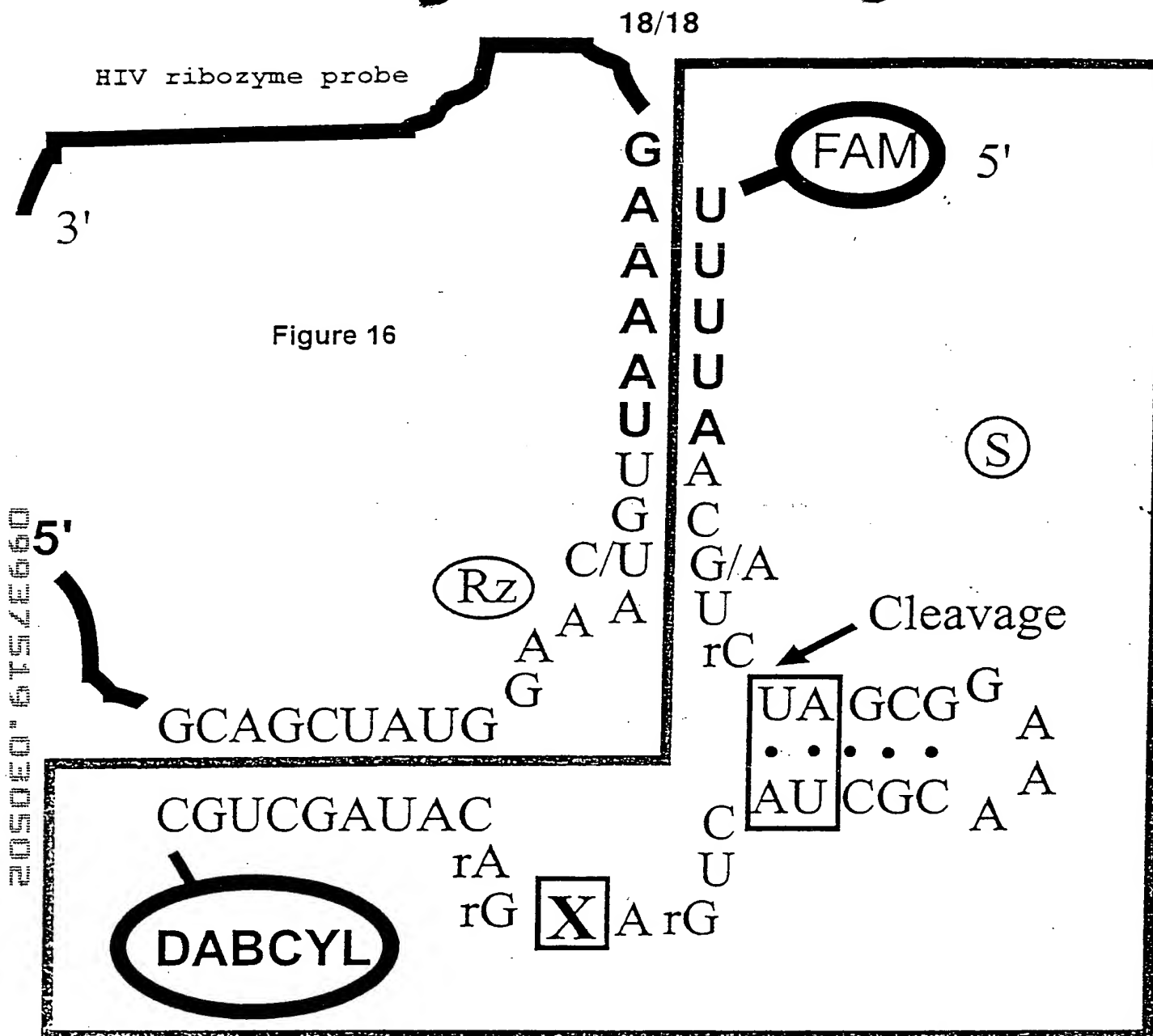
The diagram illustrates a replication fork. A replication bubble is shown with two replication forks moving in opposite directions. At each fork, the parental DNA double helix is being unwound. The leading strand is synthesized continuously towards the fork, while the lagging strand is synthesized discontinuously as Okazaki fragments away from the fork. The diagram shows the synthesis of a new DNA molecule, with the parental strands as templates and the newly synthesized strands as daughter strands. The synthesis is shown as a series of steps, with the new strands being extended by the addition of nucleotides. The diagram is labeled with 'A', 'G', 'C', and 'T' to represent the nitrogenous bases. The leading strand is labeled 'A G C' and the lagging strand is labeled 'G C'.



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00000000000000000000000000000000





X = Pyridin-4-one

r = essential ribonucleotides

important: no (C,U)-A dinucleotide in loop